EXPRESS MAIL NO: EV065007833US

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Ling, Nicholas
Gaur, Amitabh
Conlon, Paul J.
Steinman, Lawrence

(ii) TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Seed Intellectual Property Law Group PLLC
(B) STREET: 701 Fifth Avenue, Suite 6300
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 10/015,540
(B) FILING DATE: 11-DEC-2001
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Christiansen, William [illegible]
(B) REGISTRATION NUMBER: 44,[illegible]
(C) REFERENCE/DOCKET NUMBER: [illegible]

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: [illegible]
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..510

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GCG TCA CAG AAG AGA CCC TCC CAG AGG CAC GGA TCC AAG TAC CTG GCC          48
Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
 1               5                  10                  15

ACA GCA AGT ACC ATG GAC CAT GCC AGG CAT GGC TTC CTC CCA AGG CAC          96
Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
            20                  25                  30

AGA GAC ACG GGC ATC CTT GAC TCC ATC GGG CGC TTC TTT GGC GGT GAC         144
Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
        35                  40                  45

AGG GGT GCG CCA AAG CGG GGC TCT GGC AAG GAC TCA CAC CAC CCG GCA         192
Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala
    50                  55                  60

AGA ACT GCT CAC TAT GGC TCC CTG CCC CAG AAG TCA CAC GGC CGG ACC         240
Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg Thr
65                  70                  75                  80

CAA GAT GAA AAC CCC GTA GTC CAC TTC TTC AAG AAC ATT GTG ACG CCT         288
Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
                85                  90                  95

CGC ACA CCA CCC CCG TCG CAG GGA AAG GGG AGA GGA CTG TCC CTG AGC         336
Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
            100                 105                 110

AGA TTT AGC TGG GGG GCC GAA GGC CAG AGA CCA GGA TTT GGC TAC GGA         384
Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
        115                 120                 125

[illegible]                                                             432

[illegible]                                                             480

[illegible]                                                             513
```

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Ala Ser Gln Lys Arg Pro Ser Gln Arg His Gly Ser Lys Tyr Leu Ala
  1               5                  10                  15

Thr Ala Ser Thr Met Asp His Ala Arg His Gly Phe Leu Pro Arg His
            20                  25                  30

Arg Asp Thr Gly Ile Leu Asp Ser Ile Gly Arg Phe Phe Gly Gly Asp
        35                  40                  45

Arg Gly Ala Pro Lys Arg Gly Ser Gly Lys Asp Ser His His Pro Ala
    50                  55                  60

Arg Thr Ala His Tyr Gly Ser Leu Pro Gln Lys Ser His Gly Arg Thr
65                  70                  75                  80

Gln Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro
                85                  90                  95

Arg Thr Pro Pro Pro Ser Gln Gly Lys Gly Arg Gly Leu Ser Leu Ser
            100                 105                 110

Arg Phe Ser Trp Gly Ala Glu Gly Gln Arg Pro Gly Phe Gly Tyr Gly
        115                 120                 125

Gly Arg Ala Ser Asp Tyr Lys Ser Ala His Lys Gly Phe Lys Gly Val
    130                 135                 140

Asp Ala Gln Gly Thr Leu Ser Lys Ile Phe Lys Leu Gly Gly Arg Asp
145                 150                 155                 160

Ser Arg Ser Gly Ser Pro Met Ala Arg Arg
                165                 170
```

( ) INFORMATION FOR SEQ ID NO:3:

( ) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear